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RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/10/053,758

TIME: 15:47:22

Input Set : N:\Crf3\RULE60\10053758.raw Output Set: N:\CRF3\02062002\J053758.raw

SEQUENCE LISTING

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(1) GENERAL INFORMATION:
             (i) APPLICANT: Cech, Thomas R.
                             Lingner, Joachim
      6
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                             Nakamura, Toru
                             Chapman, Karen B.
      8
      9
                             Morin, Gregg B.
                             Harley, Calvin
     10
                             Andrews, William H.
     11
            (ii) TITLE OF INVENTION: Novel Telomerase
     13
     15
           (iii) NUMBER OF SEQUENCES: 225
     17
            (iv) CORRESPONDENCE ADDRESS:
                  (A) ADDRESSEE: Townsend and Townsend and Crew LLP
     18
                  (B) STREET: Two Embarcadero Center, 8th Floor
     19
     20
                   (C) CITY: San Francisco
     21
                  (D) STATE: California
                  (E) COUNTRY: United States of America
     22
     23
                  (F) ZIP: 94111
     25
             (V) COMPUTER READABLE FORM:
     26
                  (A) MEDIUM TYPE: Floppy disk
                  (B) COMPUTER: IBM PC compatible
     27
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     28
                   (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     29
     31
            (vi) CURRENT APPLICATION DATA:
                   (A) APPLICATION NUMBER: US/10/053,758
C--> 32
                   (B) FILING DATE: 18-Jan-2002
C--> 33
     59
                   (C) CLASSIFICATION: 536
     56
           (vii) PRIOR APPLICATION DATA:
                  (A) APPLICATION NUMBER: US/08/854,050
     37
                   (B) FILING DATE: 09-MAY-1997
     38
                   (A) APPLICATION NUMBER: US 08/851,843
     42
     43
                   (B) FILING DATE: 06-MAY-1997
                   (A) APPLICATION NUMBER: US 08/846,017
     47
                   (B) FILING DATE: 25-APR-1997
     48
                   (A) APPLICATION NUMBER: US 08/844,419
     52
                   (B) FILING DATE: 18-APR-1997
     53
                   (A) APPLICATION NUMBER: US 08/724,643
     57
                   (B) FILING DATE: 01-OCT-1996
     58
          (viii) ATTORNEY/AGENT INFORMATION:
     61
     62
                   (A) NAME: Apple, Randolph T.
                   (B) REGISTRATION NUMBER: 36,429
     63
                   (C) REFERENCE/DOCKET NUMBER: 015389-002930US
     64
            (ix) TELECOMMUNICATION INFORMATION:
     66
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DATE: 02/06/2002

68 (B) TELFFAX: (415) 576-0300 70 (2) INFORMATION FOR SEO ID NO: 1: 72 (1) SEQUENCE CHARACTERISTICS: 73 (A) LENGTH: 3279 base pairs 74 (B) TYPE: nucleic acid 75 (C) STRANDEDRESS: single 76 (D) TOPOLOGY: linear 77 (A) DESCRIPTION: Seo ID NO: 1: 83 AAACCCCAA AACCCCAAAA CCCCTITTAG AGCCCTICAGA ATGGAAATAT AACCTCAGTA 84 (X1) SEQUENCE DESCRIPTION: SEO ID NO: 1: 83 AAAACCCCAA AACCCCAAAA CCCCTITTAG AGCCCTICAGA ATGGAAATAT AACCTCAGTA 85 TTAATAAGCT CAGACTTTAA ATTAATATA CAAAACCTAA ATGGAGAGTA ATGTAGAAA 87 TCAAGCCGAT AACCACAAAA CCCCTITTAG AGCCCTICAGA ATGGAAATAT TAAAGAAGA 87 TCAAGCTGAT AATCATGGCA TTCACTCAGC TCTTAAGACT ATGGAAATAT AACCTCAGTA 88 TAAAACCTTA AACCATATAA TATAATATA CAAAAACCTAA ATGGAGAGAA TTAAAGAGAC 89 TAAAAACCTTA TACTTTGGA TCCAGAAAAGT TATTAAGAAA AATAATCTTG CTACACCACG 91 TATATAAGAT TTAGAAGATAT TAAAAGTTAT TACACAGACACA 93 AGCACTATAAT GAAGAAGAAT TAAAAGTTAT TACACAGAACAA 94 TATATAAGAT TATAGAAGAATAT TAAAAGTTAT TACACAGACCA 95 TAGACCAAA CTTATAGACA AATCCTTAGA ATGAAAAACAAA AATAATCTTG CAAACACCCA 96 TTAATAAACA GCTCTTTCAA CTCAAAAACCA ATAATCTTT CAAACACCAAC 97 TAGACAAAAA CTTCAATGAAA TACCTTAGT TAAACTTTCT TCAACAACACA 98 TTTATTAAACA GCTCTTTCAA CTCAAAAACCA ATTATCTTT CAAACACCAAT AACCACAAA AACCACAAAAAA	mer poulous	15, 57, 0200
(2) INFORMATION FOR SEQ ID NO: 1: (3) SEQUENCE CHARACTERISTICS: (4) LENGTH: 3279 base pairs (5) (C) STRANDEDNESS: single (6) D'OPOLOGY: linear (8) (D) TOPOLOGY: linear (9) (A) DESCRIPTION: /desc = "DNA" (1) MOLECULE TYPE: other nucleic acid (1) MOLECULE TYPE: other nucleic acid (2) (A) DESCRIPTION: /desc = "DNA" (1) SEQUENCE DESCRIPTION: SEQ ID NO: 1: 81 ARAACCCAA AACCCAAAA CCCCTITHCA AGCCCTICAGG TEGGAAATAT AACCTCAGTA (8) TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA (8) TAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA (8) TAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA (8) TAATAAGCT TAGAAGAAA TATTAAATTA CAAAACCTAA ATGGAGACAA TATAAAGAGC (8) TAATAAGCAT TAGAAGAAA TATAAAATTA TAGAAGAAA AGAAATATTTT CAACTGAGC (9) TAAAACATTTAAAAATAATT TAGCACAACAA AATATTGTTG CTACTCCACG (1) AGACTATAAA GAAAGAGATT TTAAAAATATT TAGCACAACAA AATATTGTTT CAACTGACCAC (2) AATGATAACAA CTICAATCAT TIGGATTTCA ACTTAAGGA AAAACAATTAT CAAAAGACCA (3) TAGACAAAAA CTICAAATCAT TIGGATTTCA ACTTAAGGA AAAACAAATTAT CAAAGACCACA (4) TAGACCAAAAA CTICAAATCAT TIGGATTTCA ACTTAAGGA AAATCAATTAT CAAATGACCA (5) TATATAACA GCICTTTCAA CTCAAAAGAC ATATTTCTAT CAACAGCAAT AGAACACAA (6) TAGACCAATAA AATTTTAACA AAAACCAATAA AACATTTTCAACACACAT ACTTCAAACACAT ACTTCAAACACAT TITCCAACACACAT ACTTCAACACACAT ACTTCAACACACAT ACTTCAAACACAT TITCCACACACAT ACTTCAACACACAT ACCTCACACACA		
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 3279 base pairs (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "DNA" (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: 83 ANAACCCCAA AACCCCAAAA CCCCTITTAG AGCCCTAGGA TAGGAAATAT AACCTCAGGA 75 TCAACCCAA AACCCCAAAA CCCCTITTAG AGCCCTAGGA ATGGAAATAT AACCTCAGGA 76 TCAACCTGAT AATCATGACA TAGATATATTA CAAAAACTAA ATGGAGGTTG ATGTGAAAAA 77 TCAACCTGAT AATCATGACA TCACCAGGA TCTTAAAACT TGTGAAGAAA TTAAAGAAGC 87 TAAAAACGTTG TACTCTTUGA TCCAGGAAGT TATTAGATGA AGGAGGGTTG ATGTGAAAAC 87 TAAAAACGTTG TACTCTTUGA TCCAGGAAGT TATTAGATGA AGAAACTAA ATAGGAGGTT GATCCCACG 87 AAGACCTAAT GAAGAAGAT TTAAAAATATT TGCAGGAAAA AAAATCTAT CAAAAGCAAA 87 TAAAACAAAAC CTCATATGACA AATCGTTAGT TGAACTCCTT TCATCAAGCG ATGTTTCAGC 97 TAGCACAAAAA CTTCAACTGAT TGCAGTACAA AATCAATTAG CAAAGACCCAA 97 TAGCACAAAAA CTTCAACTGAT TGGAGTTCA ACTTAAGGGA AATCAATTAG CAAAGACCCAA 97 TAGCACAAAAA CTCAACATGAT TGGAGTTCA ACTTAAGGGA AATCAATTAG CAAAGACCCAA 97 TAGACCAAAAA CTCAACATGAT TGGAGTTCA ACTTAAGGGA AATCAATTAG CAAAGACCCA 97 TAGACCAAAAA CTCACACTGATA CCCAAAAGCCA ACTCCTACA CACTAAAACCAA 101 TAGAGCAATA ACTTTGACA CAAAAAGCAAAA AGGTGGAGCA GCAGACATGC GAACCACGAT 102 CAACGTCCC AATGGAAAT AACATTCAA GACCACTCCTAC ACTAAAACTAC ACTAAAACCAA 103 ACCAACTCC GAAAGGAACT TTTCACATT TTGCAGGAACA ACCATTCTTAC ACTAAAACTACA 104 ACCTCACCAA AACCTCCAAAA ACAAATCTCAA GAAACCACA ATATTTATA GACCACACTAT 105 ACCAACCTC GAAGGAACT TCTCAAATT TTGCAGGAACACA CATACTCTAC ACTAAAACTACAA CAAAAATTCC 107 ATGGTACAACAC CACCACAACAT CAAAAACCACA ATATTTATA GAATATTCC 108 ACCAACTACA AACCATTCCT CAAAAACCACA ATATTTATA GAATATTCC 109 CAACCTCCC AATTGGAATA AAAACCACAAAAAAATTCC ACAAACATTCT CAACAACACAT TTAAAACAAAAAAAA		
(A) LENGTH: 3279 base pairs (C) STRANDEDNESS: single (C) STRANDEDNESS: single (i) MOLECULE TYPE: cher nucleic acid (ii) MOLECULE TYPE: cher nucleic acid (iii) MOLECULE TYPE: cher nucleic acid (iii) MOLECULE TYPE: cher nucleic acid (iv) SEQUENCE DESCRIPTION: /desc = "DNA" (xi) SEQUENCE DESCRIPTION: SeQ ID NO: 1: 85 THATTAGCT CAGATTITAA ATATTAATTA CARAACCTAA ATGGGGGTTG ATGTTGATAA 120 85 TTAATTAACCT CAGATTITAA ATATTAATTA CARAACCTAA ATGGGGGTTG ATGTTGATAA 120 87 TAAGAACGTAT TACATGGCA TICACTCAGC TCTTAGAACT TGTGAAGAAA TTAAAGAAGC 88 TAAAAACCTTG TACTCTTGGA TCCAGAAAGT TATTAGATGA AGAAATCAATTA CACAAAGCTC 180 TATATAAGCAT TACAAAGGAT TAAAAGTTAT TGCGCAACAA AATATTGTTG CTACTCACG 181 TATTAAAGAAT TTAGAAGATA TAAAAGTTAT TGCGCAACAA AATAATTGTTG CTACTCACG 182 AGACTATAAT GAAGAGAGTT TTAAAAGTTAT TGCAGACAAA AGAAGTATTT CAACTGAGCT 183 AGACTATAAT GAAGAGAGTT TTAAAAGTTAT TGAACTTCTT TCATCAAGCG ATGTTTCAGA 184 ATGAACCAAAA CTTCAATGAT TTGGATTTCA ACTTAAGGGA AATCAATTAG CAAAGACCCA 185 TAGACAAAAA CTTCAATGAT TGGATTTCA ACTTAAGGGA AATCAATTAG CAAAGACCAAGT 186 TAGACAAAAA CTTCAATGAA AAGCCTATCTCG ACATCAACAAATAT TAATATTCCA 186 TAGACAAAAA CTTCAATGAAA AAGCCATAAAAAAA AAGCTAATTATAA AACGTTTTTGA ACTTAGAACAAA 187 AGACTAACGA AAGTTTGGAAAAAA AGGTGGACCA GCAACACACA ATATTTTATA ACAAATATTT CAACTGGAACAAAAAAAAAA	` '	
75 (C) STRANDEDNESS: single 76 (D) TOPOLOGY: linear 78 (II) MOLECULE TYPE: other nucleic acid 9 (A) DESCRIPTION: /desc = "DNA" 81 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: 83 AAAACCCCAA AACCCCAAAA CCCCTITTAG AGCCCTGGG TTGGAAATAT AACCTCAGTA 85 TTAATAAGCT CAGATITTAA AATTAATTA TAAAACCTAA ATGGAGGTTG ATGTGGAAA 86 TTAAAAAGCT CAGATITTAA AATTAATTA TAAAACCTAA ATGGAGGTTG ATGTGGAAAA 87 TCAAGCTGAT AATCATGCGA TTCACTCAGG TCTTAAGACT TGGGAGAAA TAAAGAGAGA 87 TAAAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAAGAGT AGGAACTAA ATGAGAGAA TAAAGAGAGA 87 TAAAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAAGAGA AGAAATCAAT CTCAAAGTCA 87 TAAAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAGAGA AGAAATCAAT CTCAAAGTCA 87 TAAAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAGAGA AGAAATCAAT CTCAAAGTCA 87 TAGAACGAA CTTATTAGCA AATCCTTAGT TGCAAGAAAA AGAATCAATT CAACTGGACT 93 AGACTATAAT GAGAAAAAC TTCAATAGAC TTGAACTTCTT TCAACTAAGC ATGTTTCAGA 94 TATATAACA GCTCTTTCAA CTCAAAAGCA ATTATTCTTT CAACAAGCG ATGTTTCAGA 95 TATATTAACA GCTCTTTCAA CTCAAAAAGCA ATATTCTTT TCAACAAGCG ATGTTTCAGA 96 TTTATTAACA GCTCTTTCAA CTCAAAAAGCA ACATTCTTCTT CAAGACGAAT GAACCACAT 101 TAGACAAATA AGCACTTTACAA CAACAACAA AAAACAATATAT TAATATTCCA 102 AGCCAACGAAT AAGTTGGACA AAAAGCAAAAA CAATATCTTCTT CAACAACCAT 103 AGCCAACGAAT AAGTTTGACA AAAAGCAAAAA CAATACATTAT TACAATATCCA 104 AGGTGAACAA AACCTCCAAAAAACAA AAAACAATACA TCCAAAAACAA CAATACATCAA CAAAACACAAA ACAATATCT TAAAAAACAA CAAATACAATACA AAAACACAAA AAAAATATTA AACAATATCA AAAAACATACA CAAGAACAAA ACAATATCT TAAAAAACA TAGAAAAAAAAAA		
75 (C) STRANDEDNESS: single (i) MOLECULE TYPE: other nucleic acid (y) (A) DESCRIPTION: /desc = "DNA" 81 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: 83 AAAACCCCAA AACCCCAAAA CCCCTTITAA AGCCCTAGA TAGGAGATTA AACCTCAGTA 85 TTAATAAGGT CAGATTITAA ATATTAATTA CAAAACCTAA ATGGAGAGTTA ATCTTGATAA 87 TCAAAGCTGA AATCATGGCA TICACTCAGC TCTTAAGAGTA TGTGAGAGAA TTAAGAGAGC 88 TAAAAACGTTG TACTCTGGA TCCACTAGAG TCTTAAGAGAT TGTGAGAGAA TTAAGAGAGC 89 TAAAAACGTTG TACTCTTGGA TCCACTAGAG TCTTAAGAGAT TGTGAGAGAA TTAAGAGAGC 80 TAAAAACGTTG TACTCTTGGA TCCAGAGAGA TTATTAGATGA AGAAACTAAT CTCAAAGTCA 81 TTATAAAGAT TTAGAAGATA TAAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG 82 AAGACTAAAA CTTCAATGAA ATGCTTAGT TGCAGCAGAC AATATTGTTG CAAGACCCA 80 TAATATAACA CTTCAATGAT TTGGATTTCA ACTTAAGGGA ATCAATTGTTG CAAGACCCA 81 TAGACAAAAA CTTCAATGAT TTGGATTTCA ACTTAAGGGA ATCAATTGTTG CAAGACCCCA 82 TAGACCAAAAA CTTCAATGAT TTGGATTTCA ACTTAAGGGA ATCAATTACA CAAGACCCCA 83 TAGACCAAAAA CTTCAATGAT TTGGATTTCA ACTTAAGGGA AACCAATT TAAAATTCT 84 TAGACAAAAA AGCTTTCAA CACAAAGACAAAA AGCTGCAGCA CAAAGACCCCA 85 TATTATAACA GCTCTTTCAA CACAAAGACACA 86 TTATTATAACA GCTCTTTCAA CACAAAGACACA 87 TAGACCAAAAA ATTGGAATT TTGCAATGAAA AGCTCTCTT CAAGAGACACACT 88 TAGACCACTA CACTCCAAAA AAAACCAAAA AGCTCCTAC ACTAAAATATT TAAATATTCA 89 TTAATTAACA GCTCTTTCAA CACAAAGACACAAA AGCTCTCTAC ACTAAAATATT TAAATATTCA 80 CAACCTGCC AATTGGAATA ATATGAAATC AGAACCACAA ATATTTTATT TAAATATTCA 80 CAACCTGCC AATTGGAATA ATATGAAATC AGAACCAGA ATATTTTATT TGCACACACAT 80 CAACCTGCC AATTGGAATA ATATGAAATC AGAACCAGA ATATTTATTATT TAAACACTCCATT 80 CAACCTGCC AATTGGAATA ATATGAAATC AGAACCAGA ATATTTATTAT GCACCACATT 80 CAACCTGCC AATTGGAATA ATATGAAATC AGAACCAGA ATATTATTAT TAAACACTCCATT 81 AACCAAAGAATA ATACAATTCA CAAAAACCTTC CTCAGAAAA ACAATTTCC 107 ATACTCAAC TACAATTGA TAAATAAAAAC TAGAACACAA AAAACTTTC AGAATAAATA CAAAACTTCA TAAATAAAAAC AGAACATTC CTCAAAAAACTTC AAAAAACTTC AAAAAAACTAC AAAAACTTTC TAAAAAAAA	, ,	
(i) MOLECULE TYPE: other nucleic acid (ii) MOLECULE TYPE: other nucleic acid (ii) MOLECULE TYPE: other nucleic acid (iii) AAACACCAA AACCCCAAAA ACCCTTAGA TOCACAAAACCTAA ATGGAAATAT AACCTCAACAAAAACCTAAAAACAAAAAAAAAA		
78 (1) MOLECULE TYPE: other nucleic acid 79 (A) DESCRIPTION: /desc = "DNA" 81 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: 83 AAAACCCCAA AACCCCAAAA CCCCTTTTAG ATATTAATTA 85 TTAATAAGCT CAGATTTTAA ATATTAATTA LAAAACCTAA ATGGAGTTG ATGTTATAA 87 TCAAGCTGAT AATCATGGCA TCACTCAGC TCTTAAGACT TGTGAAGAAA TTAAAGAGC 180 87 TAAAAGTT TACGAAGATA TTAAAATATT TGCACCAACA ATATTTTGTG CTACTCACG 300 81 TATATAAGAT TTAGAAGATA TTAAAATATT TGCGCAGACA ATATTTTTCTTT CCACCACG 300 83 AGACTATAAT GAAGAGAT TTAAAATTAT TGCGCAGACA ATATTTTCTT CCACCACG 300 84 ATAGATCGAA CTTATTGACA ATGCTTATT TGCGCAGACA ATATTTCTT CAACAGCC 420 85 ATAGATCGAA CTTAATGAC AATGCTTACT TGCACAGACA ATATTTCTT CAACAGCC 420 86 TTATTATACA GCTCTAAAACA ATGCTTTTT TCAACAACACA ATATTTCTTCACACCCACACACA		
(A) DESCRIPTION:		
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85 TTAATAAGCT CAGATTITAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA 120 87 TCAAGCTGAT AATCATGGCA TCCACGC TCTTAAGACT TGTGAAGAAA TTAAAGAAGC 180 89 TAAAACGTGT TACCTCTGGA TCCACGAAGT TATTAGATCA AGAAATCAAT CTCAAACTCA 240 91 TTATAAAGAT TTAGAAGATA TTAAAAATATT TGCGCAGACA AATATTGTTG CTCACACGG 360 93 AGACTATAAT GAAGAAGAT TTAAAATATT TGCACGAGAAAA GAACTATTTT CAACTGGACT 360 95 AATGATCGAA CTTATTGACA AATGCTTACT TGAACTCTT TCACTCAAGCG ATGTTTCAGA 420 97 TAGACCAAAAA CTTCAATGAT TTGGATTCAA ACTCAATCTT TCACTCAAGCG ATGTTTCAGA 420 98 TTAATTACAC ACTCAATGAT TTGGATTCA ACTTAAGGGA AATCAATTAG CAAAGACCCA 480 99 TTTATTAACA GCTCTTTCAA CTCAAAAGCA GTATTTCTT CAACAGCGAAT GGAACCAAGT 540 101 TAGAGCAATA ATTGGAAATG AGCTCTTCCC ACATCTCTAC ACCTAAATATT TAATATTCCA 660 103 GCCAACTTCT GAAGGAACT TTGTTCAATT TTGCGGGAAT AACGTTTTTG ATCATTTGAA 660 105 AGTCAACGAT AAGTTTAGACA AAAACCAAA AGGTGGACCA GCAGACCATGA ATGAACCTCG 720 107 ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGACAA GATCACTTC TCAACACAAT 780 109 CAACGTGCCG AATTGGAAT ACAATGTCAA GAATGACAA GATCACTTC TCAACACACAT 780 101 TAATAGAAAT AACCAATTCT TCAAAAAGCA TAATATTAAT GCACTCAATT 480 111 TAATAGAAAT AACCAATTCT TCAAAAAACCA TAATATTAAT AGAATTTAATT GCACTCAATT 780 112 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATAT AGAATTTAATA GAATTAGAAA 960 113 AGCGATGGAC AGACTCAGA CGATATTCAC GAATATTCAC GAATATATTC AGATTTAATA GAATTAGAAA 960 114 ACAAAAAAATC TACTATTTAA CAAAATCTG TCCTCTCCA GAAAATTGCC GGGAACGGAA 1080 115 AAACACAATA TACCAACTG ATAATAAAAC TAGAGAGAAA AACCCAAAA AACAATATTC 1020 117 TAACTTCAAC TACTATTAA CAAAATCTG TCCTCTCCA GAAAATTCC AAAAAAAAAT CTCACAACGA TAATAAAAAC TAGAGAATA ACAAACTGA ATATTATATA CAAAAACTGA ACAAACATA TCCACAACTG ATAATAAAAC TAGAGAAAA AACCAATATTC ACAAACAGA TACTATTAAA CAAAACATTC TCCTCTCCA GAAAATTTC AAAAAAAAAA	92 ANARCCCON ARCCCCAAA CCCCT	TTTAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA 60
87 TCAAGCTGAT AATCATGGCA TCACTCAGC TCTTAAGACT TGTGAAGAAA TTAAACAGAC 240 1 TAAAACGATG TACTCTTGGA TCCAGAAGTA TATTAGATGA AGAAATCAAT CTCAAAGTCA 240 1 TATTAGAAGAT TTAGAAGATA TTAAAAATATT TGCGCAGACA AATATTGTTG CAACTCCACG 360 3 AGACTATAAT GAAGAAGAT TTAAAAATATT TGCAGAGAAA AGAGTATTTT CAACTGGACT 360 3 AGACTATAAT GAAGAAGAT TTAAAAGATATT TGCAAGAAAA GAAGTATTTT CAACTGGACT 360 3 AGACTACAAAA GAAGAAATATT TAAAAATATT TGCAAGAAAA GAAGTATTTT CAACTGGACT 360 3 AGACTACAAAAA GATTAATTAGAA AATCACTTAAT TGCAACAAAA GAAGACCAA 420	95 TENATA ACCT CAGATTTTAA ATATT	AATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA 120
89 TAAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA 240 91 TTATAAAGAAT TTAGAAAGATA TTAGAAAGATA TGCGCAGACA AATATTGTG CTACTCCACG 300 93 AGACTATAAT GAAGAAGATA TTAAAATAAT TGCGCAGACA AATATTGTG CAACTCCACG 360 95 AATGATCAAA CTTATTGACA AATGCTTAGT TGCAAGAAAA GAAGTATTTT CAACTGAACCT 420 97 TAGACAAAAAA CTTCAATGAT TTGGATTCA ACTTAAAGGA AATCAATTAG CAAAGACCCA 480 101 TAGAGCAATG ATTGGAAAAGC ACTATTCA ACTAAAGAGA AATCAATTAT TAATATTCCA 600 101 TAGAGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTCA ACTAAAATAT TAATATTCCA 600 103 GCGAACCTTC GAAGGAACTC TTGTCCAATT TGGGGGGAC AACGACCAAGT 700 104 AGTGTAGACGAT AAGTTTGACA AAAAGCAAAA AGGTGGGACC AGCACACAAGT 720 105 AAGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGC GCAGACCATGA ATGAACCTC 720 107 ATGTGGACA AACTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACCATGA ATGAACCTC 720 108 CAACGTGCCG AATTGGAAA ACAAGCAAAA AGGTGGAGCA GCAGACCATGA ATGAACCTC 720 109 CAACGTGCCG AATTGGAATA ATATGAAAAC AGAACACAACATTC TCAAAAAACCA ACAATATTT GCACTCAATT 800 111 TAATAGAAAAT AACCAAATTCT TCAAAAAACCA TGAGTTTTGT AGAACAAAA ACAAATATTC 900 112 AGCAATGAAC AGACCACAACTCT TCAAAAAACCA TGAGTTTTAGT AGAATATATC AGAATTAATT GAATTTAATT GAAATATTC 1020 113 ACCACAAACAC ACTGA TAAAAAAAC TGCCAACAA TGCACAACAT TCCAAAAACCA ACAATATTTC 1020 114 TAACTCCAAC TACTATTTAA CAAAAACCA TAGAAAAAC AGAACATTCT TCAACAACACT TTTGACACAACACA	97 TCAACCTCAT AATCATCCCA TTCAC	TCAGC TCTTAAGACT TGTGAAGAAA TTAAAGAAGC 180
91 TTATAAAGAT TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG 360 93 AGACTATAAT GAAGAAGATT TTAAAAGTTAT TGCAAGAAAA GAAGTATTT CAACTGGACT 360 95 AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTCTT TCATCAAGGG ATGTTTCAGA 420 97 TAGACAAAAA CTTCAATGAT TTGGATTCA ACTTAAGGGA AATCAATTAG CAAAGACCCA 480 99 TTAATTAACA GCTCTTCCAA CCCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT 540 101 TAGAGGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAAATAT TAATATTCCA 660 103 GCGAACTTCT GAAGGAATG AGCTCTTCCAA ACATCTCTAC ACTAAAATATT TAATATTCGA 660 105 AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA GCAGCATGA ATGAACCTCG AATTGGAAAT ACAATGCAA AGGTGCAG ACATCTTTTG ATCATTTTGA 660 107 CAACGTGCCG AATTGGAAAT ACAATGCAA AGGAGAAA GATCACTTTC TCAACAACAT 780 108 CAACGTGCCG AATTGGAAAT ATAGAAATC AGGACCAGA ATATTTATT GCACCTCATT 840 110 TAATAGAAAT AACCAATTCT TCAAAAAACCA TGAGTTTGTG AGTAACAAAA ACAATATTC 111 TAATAGAAAT AACCAATTCT TCAAAAAACCA TGAGTTTTGTG AGTAACAAAA ACAATATTC 112 GAACCTAAAA GATAAGGTA TCAAAAAAAC TGCCTACATC ACTTGAGAAAA ACAATATTC 113 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGAATTTAAAAAA CAAAATATTC 114 TAACTTCAAC TACTATTTAA CAAAAATCTTG TCCCTACCAC TTTGAGAAAA ACAATATTC 115 TAACTTCAAC TACTATTAA CAAAAATCTTG TCCCTTCCCA GAAAATTGC GGGAACGGAA 1080 116 ACAAAAAAATC CACAAACTG ATAATAAAAC TAGAGAACCT AGAAATTTCA CAAAAACTTG TACAAAAAAAT TCATATTTAA CAAAAATCTTG TCCTTCCCA GAAAATTTCA CAAAAACTTA ACAAAAATCTTG TCCTTCTCCA GAAAATTTCA AATTTTCTA 1200 123 CAATATACC TACCAAACTG ATAATAAAAC TAGAGAACCT AAGAAATTTC AAAAAAACTTA 1200 124 CAATATACA AGAGAAATT CATGGATGA ACTCATTCAC AAAAAATTTT CAAGAAAAT 11020 125 TAAGAAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC AAAAAATTTT TCATGAGAA 1140 121 CGTCGTCC CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTTTTTTTA 1380 129 TTTTGATCAC GAAAACTCT ACCTCTTATG GAAATTGCC CAACAGAAAA GTTTTTTTTATTA 1380 129 TTTTGATCAC GAAAACTCT ACCTCTTATG GAAATTGCC CAACAGAAAA GTTTTTTTTTATTA 1380 129 GACTTTCAAT AAGAAACTT ACCGCAAGAA AAAACTGCC CGAACAGAAAA TTTTTATTA 1380 131 CGTCGTCCC CTGATTAGAT GATTTTTCAT TGTCACCAGA TATTTACCAACTT TACCAAAATTA CACAACTAT TCACAACTAT TCACAACTAT TCACAACTAT TCACAACTAT TCACA	90 TAAAACCTTC TACTCTTGGA TCCAG	AAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA 240
93 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTT CAACTGGACT 95 AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTTCTT TCATCAAGCG ATGTTTCAGA 97 TAGACAAAAA CTTCAATGAT TTGGATTTCA ACTTAATGGA AATCAATTAG CAAGAACCCA 98 TTATTAACA GCTCTTTCAA CTCAAAGCA GTATTCTT CAAGACGAAT GGAACCCA 101 TAGAGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAAATATT TAATATTCCA 103 GCGAACTTCT GAAGGAACT TTGTCAATT TTGCGGGAAT AACGTTTTTG ATCATTTGAA 105 AGTCAACGAT AAGTTTGACA AAAGCAAAA AGGTGGACCA GCAGACATGA ATCAACTCT 107 ATGTTGATCA ACCTGCAAAT ACATGTCAA GAAGCACAA AAAGCCAAAA AGGTGGACCA GCAGACATGA ATGAACCTC 107 ATGTTGATCA ACCTGCAAAT ACAATGCTAA GAAGCACAA AAAGCAAAA AGGTGGACCA GCAGACATGA ATGAACCTC 108 CAACGAGCCA AAATCCT TCAAAAAACAA AACGAACACAA ATATTTATT GCAACAACAT 109 CAACGTGCCC AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTATT GCACTCATT 111 TAATAGAAAT AACCAATTCT TCAAAAAGCA TGACTTTCTC AGAACACAT 780 112 AGCCATGGAC AGAGCTCAGA CAATTCCC GAATATTCC AGAACACAAA ACAATATTTC 113 AGCCATGGAC AGAGCTCAGA CAATTCCC GAATATTCC AGAATATTC AGAATTATAA GAATTAGAAAA 114 GAACAAAAAACT TACAATTAA CAAAATCTTG TCCTCTCCCA GAAAATTGAAAAAAAAAA	O1 TEATA A A CAT TEACA A CATA TEAA	ATATT TGCGCAGACA AATATTGTTG CTACTCCACG 300
95 AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTTCTT TCATCAAGCG ATGTTTCAGA 97 TTAGACCAAAAA CTTCAATGAT TTGGATTTCA ACTTAAGGGA AATCAATTAG CAAAGACCCA 98 TTTATTAACA GCTCTTTCAA CTCAAAAGCA GTATTTCTTT CAAGAGCAAT GGAACCAAGT 101 TAGAGCAATA ATTGGAAATA ACCTCTTCCG ACATCTCTAC ACTAAAATAT TAATATTCCA 103 GCGAACTTCT GAAGGAACT ACATCTCTAC ACTTAAATATT TAATATTCCA 105 AGTCAACGAT AGGTTTGACA AAAAGCAAAA AGGTGGAACCAAGT ATGATTTGAAC ACTCAAATATT TAATATTCCA 106 AGTCAACGAT ACATTGGAAAT ACAATGTCAA GAATGACACAGA ATGATTTTGAA ATGAACCTCG 107 ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA AGGTGAACAGA ATGAACACACT 109 CAACGTGCCG AATTGGAATA ATATGAAAAT AAAAGCAAAA AGAACCAGA ATATTTTATT GCACCACAT 110 CAACGTGCCG AATTGGAATA ATATGAAAAT AAAAGCAAAA AGAACAAAA ACAAATATTC 111 TAATAGAAAT ACCAATTCT TCAAAAAAGCA TGACTTTCTG AGTAACAAAA ACAAATATTC 112 GAAGCATAGAA GAATAGGAATA TCAAAAAACCA TGACTTCTG AGTAACAAAA ACAAATATTC 113 AGCCATGACA AGAACTCTA CGAATATTCAC GAATATTCA AGATTTAATA GAAATTAGAAA 114 ACACTACAACA ACAAAAACTTG TCCTCTCCA GAAAATTGGC GGGAACGGAA 115 GAAGCATAAA GAATATATAA CAAAAATCTTG TCCTCTCCA GAAAATTGGC GGGAACGGAA 110 ACAAAAAAATC GAAAAACTCA TAAATAAAAC TAGAGAAGAA ACAATATTCA AAATTTCTAA 120 CTCTTTAGC TACCCAACTG ATAATAAAAA CGTCACCACAA TTTATTAATA AATTTTCTA 120 CTCTTTAGC TACCCAACTG ATAATAAAAA CGTCACCACAA TTTATAATA AATTTTCTA 120 CTCTTTAGC TACCCAACTG ATAATAAAAT CGTCACACAA TTTAATATAA AATTTTTCTA 120 CTCTTTAGC CCCAAACTG ATAATAAAAC CGTCACACAA TTTATTAATA AATTTTTCTA 120 TTTTGATCAC CCCAAACTG ATAATAAAAT CGTCACACAA TTTATTAATA AATTTTTTAT 120 TTTTTGATCAC CCCAAACTG ATAATAAAAT CGTCACCACA TTTTTATATA TAATTAATA AATTTTTTAT 121 TTTTTGATCAC CCCCAAACTG ATAATAAAAT CGTCACCAG CACACAAATTTTTATTATA 122 TTTTTGATCAC CCCCAAACTC ACTCTTTTTG GAAATTCCC CGATGGATAT TCGCAGAAC TTTTTTTATA 123 AACCTATTAC TACCAACTG ATATTTCAT TGTCACCAG CAACACAAAA CTTTTTTTATA 123 AACCTATTAC TACCAAACTC ACTCTTTTTTA TGTCACCAG CAACACAAAA CTTTTTTTATATATATATATATATAA CAAAAATTCA TACGAAAAAA ACACACTCT ACAGAAAAA ACACACAAAA ACACACAAAAA ACACACAAAAA ACACACAAAAA ACACACAAAAAA	O2 ACACTATAAT CAACAACATT TTAAA	GTTAT TGCAAGAAAA GAAGTATTTT CAACTGGACT 360
97 TAGACAAAAA CTTCAATGAT TTGGATTTCA ACTTAAGGGA AATCAATTAG CAAAGACCCA 480 99 TITATTAACA GCTCTTTCAA CTCAAAAGCA GTATTTCTTT CAAGACGAAT GAACCACAGT 540 101 TAGAGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA 600 103 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTGA ATCATTTGAA 660 105 AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG 720 107 ATGTTGATCA ACCTGCAAAT ACAATCTCAA GAATCAGAAA GATCACTTT TCAACAACAT 780 109 CAACGTGCCG ACATTGGAATA ACAATCTCAA GAATCAGAAA AGAACCAGA ATATTTTAT GCACTCATTT 840 111 TAATAGAAAT AACCAATTCT TCAAAAAAGCA TGACTTTCT GACACAACAT 780 113 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATAATATC AGAATTATTAT GCACTCATTT 840 114 TAATAGAAAT AACCAATTCT TCAAAAAACA TGACTTTCT ACAACAAAA ACAATATTTC 900 115 GAAGCTAAAA GATAAGGTTA TCGAAAAAAA TGCACTCATTT AGAATTATATA GAATTAAAAA CAAATATTC 900 116 GAAGCTAAAA GATAAGGTTA TCGAAAAAAAT TGCCTACATC CTTGAGAAAA CAAAATATTT 1020 117 TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTTCCA GAAAAATTGC GGGAACGGAA 1140 119 ACAAAAAATC GAAAACTTG TAAATAAAAC TAGAGAAGAA AACTGGAAG ACTGAAGATTT 1020 112 GCTGTTTAGC TACACAACTG ATAATAAAAC TAGAGAAGAA AACTGGAAG ACTCATGAAGA 1140 121 GCTGTTTAGC TACACAACTG ATAATAAAAC CAGACATCA ACAAAATTTC AAAAAATTC 1200 122 GAATATACTC CCCAAAGACT TTTTGACTGG AGAAACCGT AACAAATTTC AAAAAAAATT 1200 123 CAATATACTC CCCAAAGACT TTTTGACTGG AGAAACCGT AACAAATTTC AAAAAAAATT 1200 124 GATCAATACA AGAGAAATT CATGAAGCA GGTTGAGACC TCTGCAAAAC ATTTTATTA 1380 125 TAAGAAAATAT CAGGAACTAA ACAAGCATGA ACTCATTCAC AAAAACTTAT TTGCTGAGAA 1320 127 GATCAATACA AGAGAAATT CATGAAGCA GGTTGAGACC TCTGCAAAAC ATTTTATTA 1380 128 TTTTGATCAC GAAAACATCT ACGGATGA ACAACCATTA ACAAGAATTTC CAAAAACTTAT TTGCAGAAA ACCTCCAA 1500 133 AACCTATTAC TACAGAAACA TATTTGGGA CATTTTCTA TGCACAAAAA GTTTATTATA 1340 140 GAAGATTAC TACAGAAACA TATTTGGGA CATTTTCTA TGCACAAAAA GTTACTCCAA 1500 134 TTTGGATTAC CCCGAGAAAC TAATTTCGA CAGACGATAT ACCGAAGAAA ACTTCTCCA ACAAAATTAC 1680 143 TTTTGAATTC TACAGAAACA TAATTTCGA CCGAGGAAAA ACTTCTCCA ACAAATTAC 1740 141 GAAGTTATTC GAACACATA ACCAAAACT CTTCTTTTGCA ACAAAATTAC TACAAAATAC 1740 144 GAAGTTATTC	05 ANTCATCOAN CTTATTCACA AATCC	TTAGT TGAACTTCTT TCATCAAGCG ATGTTTCAGA 420
99 TTTATTAACA GCTCTTTCAA CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT 101 TAGAGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAATATT TAATATTCCA 600 103 GCGAACTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGATTTTG ATCATTTCCA 105 AGTCAACGAT AACTTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG 107 ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA GGTGGAGCA GCAGACATGA ATGAACCTCG 108 CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCACA ATATTTTATT GCACTCATTT 111 TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC 112 GAAGCTAGAA GAACATCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC 113 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGAATTAATA GAATTAGAAA 114 GAAGCTAAAA GATAAGATTA TCGAAAAAAT TGCCTACATG CTTGAGAAAA TCAAAGATTT 115 GAAGCTAAAA GATAAGATTA TCGAAAAAAT TGCCTACATG CTTGAGAAAA TCAAAGATTT 116 GAAGAATAC TACTATTTAA CAAAAATCTTG TCCTCTCCCA GAAAATTGCC GGGAACGGAA 1080 117 TAACTTCAAC TACTATTTAA CAAAAATCTTG TCCTCTTCCA GAAAATTGCC GGGAACGGAA 1140 118 ACAAAAAATC TACACAACTG ATAATAAAAC TAGAGAAGAA AAGTCGAAGA ACTAGAAGA 1140 119 ACAAAAAATC CCCCAAAACTG ATAATAAAAC TAGAGAAGAA AAGTCGAAGA ACTATAGAAA 1140 112 GCTGTTTAGC TACACAACTG ATAATAAAAC CGTCACACAA TTTATTATAATG AATTTTCTA 1200 113 ACAATATACTC CCCAAAGACT TTTTGACTGG AAGAACCGT AAGAATTTTC AAAAAAACTTA 1200 114 GAACAAAAATT CACACAACTG ATAATAAAAC CATGAGACCG AAGAAATATT TCCTTCAGAGAA 1200 115 TAGAGAAATAT CACACAACTG ATAATAAAAC CATGAGACCG AACAACACAA ACAACATTA TCCTTCAGAGAA 1200 116 GATCATTACA CAAAACATCT ACGTCTTATG GAAAATTGCC CAAAGAATTTT TCTTTATTA 1380 117 TTTGATCAC CACAAACATC ACGTCTTATG GAAATTGCC CAACGGAAAA GTTTTTTATTA 1380 118 CGTCCTCTCC CTGATTAGAT GATTTTTCTA TGTCACCAG CAACAGAAAA GTTACTCCAA 1500 118 AACCTATTAC TACAGAAACAT TAGACTCAAAACT TAGACCATCATAT ACCGAAGAAAA ACTACTTAC TACAGAAACAT TAGACCAAACTT TAGACAAACAT TAGACAAACAT TAGACAAACAT TAGACAAACAT TAGACAAACAT TAGACACAAACAT TAGACAAACAT TAATTTCGAAAAACAAACATTAC AACAAACATAC AACAAATTAC AACAAATTAC AACAAAATTAC AACAAAACATAC AACAAACA	95 AAIGAICGAA CITATIONEN IMIGE	TTTCA ACTTAAGGGA AATCAATTAG CAAAGACCCA 480
101 TAGAGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA 600 103 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGGGGGAAT AACGTTTTTTG ATCATTTGAA 660 105 AGTCAACGAT AAGGTTTGACA AAAAGCAAAA AAGGCAGAA GGAGGACATGA ATGAACCTCG 720 107 ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA GATCACTTTC TCAACAACAT 780 108 CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT 840 109 CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT 840 111 TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTC 900 113 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA GAATTAGAAA 960 115 GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAAG TCAAAAGATTT 1020 117 TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTCACA GAAAATTGGC GGGAAACGGA 1080 119 ACAAAAAAAC GAAAACTTGA TAAATAAAAC TAGAGAAGA ACAACACGAG ATTTTTTAATA CAATTAGAAA 1140 121 GCTGTTTAGC TACACAACTG ATAATAAAAC CGTCACACAA TTTTATTAATA AATTTTCTA 1200 122 CAATATACC CCCAAAGACT TTTTGACTGG AAGAAACGT AAGAATTTT TAATAAGAAAGT 1260 123 CAATATACT CCCAAAGACT TTTTGACTGG AAGAACCGA ACTCATTCTC AAAAACTTTT TCAAAGAAAGT 1260 125 TAAGAAAATA GAGGAAAAA ACAAGCATGA ACTCATTCAC AAAAACTTTT TCAATGAGA 1320 127 GATCAATACA AGAGAAAAT CATGGATGCA GGTTGAGAC TCTGCAAAGC ATTTTTTATT 1380 129 TTTTGATCAC GAAAACACT ACGTCTTATG GAAATTGCC CGATGGATAT TCGAGGATCT 1440 131 CGTCGTCTCG CTGATTAGAT GATTTTTCTA TGTCACCGAC CAACAGAAAAA GTTACTCCAA 1500 133 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATATT GAAAACGTAT TCGAGGACTT 1560 134 AAGAGGAA ACGCTTGCTG AGGTCCAAGA AAAACGGTT GAACAGAATGA AAAACTTCCAA 1500 135 AAAGAAGAA ACGCTTGCTG AGGTCCAAGA AAAACGGTT GAACAGAATGA AAAACTCCAA 1560 136 CAAATGGAAG ACGCTTGCTG AGGTCCAAGA AAAACGGTT GAACAGAATGA AAAACTTCCAA 1680 137 TGGATTTCAA AAGAGAATG TAAACAACAC TCAAAAATAC 1740 138 GACTTCAAT AAGAAACAC TCAAAAACT TAAAATCCAA AAAAACTAC TACAAAAATC 1740 139 GACTTCAAT AACAACAC TAAAACTATA ACCGAAGAAAC ACCAAAAATTA CTACAAAATC 1680 139 GACTTCAAT AACAGAAC ATATTTCGAA AAAACTACCA AAAAACTAC TACAAAAAC 1740 141 GAAGTTTTCA CGCGAAAC TCAAAACTAC AAAAACTAC TACAAAAACT TAAAACAGAC AACAAAACTAC AACAAAACTAC AACAAAACT TAAAACAGAG AACAAAACT	QQ TTTATTAACA CCTCTTTCAA CTCAA	AAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT 540
103 GCGAACTTCT GAAGGAACT TTGTTCAATT TTGCGGGAAT AACGTTTTTG ATCATTTTGAA 660 105 AGTCAACGAT AAGTTTGACA AAAACCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG 720 107 ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA GGTCACTTTC TCAACACACAT 780 108 CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTATT GCACTCATTT 840 111 TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGT GACTCATTT 6ACCACACAT 780 113 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGAATTAATA GAATTAGAAA 790 115 GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAA ACAATATTTC 900 117 TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTCACA GAAAAATTG CAGAACATT 1020 118 ACAAAAAAATC GAAAAATCTTAAAAAAC TAGAGAACAA ACAATATTCA GAATTAATA GAATTAGAAA 110 119 ACAAAAAAATC GAAAAATCTA TAAATAAAAC TAGAGAAGAA ACAACAGAAA ACAACATTAT 1020 110 ACAAAAAAATC CACAACTG ATAATAAAAC CAGAAACCGT AAGAAATTTC AAAAAAAATTC AAAAAAAATC CACAACACA TTTATTAATA AATTTCTA 1200 112 GCTGTTTAGC TACACAACAC ATAATAAAAC CGTCAACAA TTTATTAATA AATTTCTA 1200 112 GCAATACACA AGGAAAAAT CAAGACATCA ACAAGCATGA ACTCACTCAC AAAAACTTTT AAAAGAAAAT 1260 112 TATGAATACA AGAGAAAATA CATGGAAGAA ACAACCGT AAGAAACTTT TGCTTGAGAA 1320 112 GATCAATACA AGAGAAAATA CATGGAATGA GGTTCAAGAC TCTGCAAAGA ATTTTTATTA 1380 119 TTTGAACCA GAAAACACT ACGTCTTATG GAAATTGCC CGATGGATAT TCGCAGACCT 1440 131 CGTCGTCTCG CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA 133 AACCTATTAC TACAGAAAGA ATATTTGGA CGTCAATAA AAAATTCCAA AAAACTCCCA 1500 133 AACCTATTAC TACAGAAAGA ATATTTGGA CGTCAATAA AAAATTCCAA AAAACTCCCA 1620 134 TTGGATTTGC CCTGGAAAC TAGACCTAA AAAACGGTT GAACAGAGAAA ACGCCTTCCAAGA AAAACGGTT GAACAAGAAACA TTCAAAAACA 1620 135 AAAGAAGAA ACCTCCACT TAATGCATAA AAAAACTGCA TACAAAATTA CTACAAAATC 1620 136 GAATTTGCA CCTGGAAAAC TAAACAGAA AAAACAGGTT GAACAAGAAACT TACAAAATAC 1620 137 TGGATTTGC CCTGGAAAC TAAACAGAA AAAACAGGTT GAACAAGAAACT TACAAAATAC 1620 138 GACTTCAAT AAGAAGAA AAAACATC AAAAACTATA ACCAAAATTA ACCAAAACTT TAAACAGAG AAAAACTATC AAAAATTAC TACAAAAACT TAAACAGAG AACAAAACT TAAAACAGAG AAAAACTACC AACAAAACT TAAACAAACT TAAACAAAACT TAAAAAAACT TAAAAAAAA	101 TACACCAATC ATTGGAAATG AGCT	CCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA 600
105 AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG 720 107 ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA GATCACTTC TCAAACAACAT 780 109 CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT 840 111 TAATAGAAAT AACCAATTCT TCAAAAAACCA TGAGACCAGA ATATTTTATT GCACTCATTT 840 113 ACCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATC AGATACAAAA ACAATATTTC 900 114 ACAACAACA GACACTCACA CGATATTCAC GAATATATC AGATTTAATA GAATTAGAAAA 960 115 GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT 1020 117 TAACTTCAAC TACTATTAA CAAAATCTTG TCCTCTTCCA GAAAATTGCC GGGAACGGAA 1080 119 ACAAAAAAATC GAAAACTTG ATAAATAAAAC TAGAGAAAAA ACAATATTTCTA ACTATGAGAA AGAACATCTA TACAAAAAACT TTTGACTGG AAGAACTTCA AAAAACTTCA AACAACACT ATAAAAAAC CGTCACACAA TTTATTAATAG AAATTTTCTTA 1200 123 CAATATACCA CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAACTTTA TGCTTGAGAA 1220 125 TAAGAAAATAT GTGGAACTAA ACAAGCATGA ACTACTACA AAAAACTTAT TGCTTGAGAA 1220 127 GATCAATACA AGAGAACATAT CATGGATGCA GGTTGAGACC TCTGCAAAAG ATTTTATTA 1380 129 TTTTGACTCG GAAAACATCT ACCGCACAAA TATTTCCAC CAACAGAAAA GTTACACAACTG ATAATTTCATA GAAATTTCC CGATGGAAAC ATTTTTATTA 1380 129 TTTTGATCAC CTGAATAGA ACACCTTATTCA GAAATTGCTC CGATGGAATA TCGCAGGACTT 1440 131 CGTCGTCTCG CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACCCAA 1500 133 AACCTATTAC TACAGAACAA ATATTTCGA CGCTAATTAT GAAAATTCCAA TCGCAGACTT 1440 134 TGGATTTCA TCCAGAAACA ATATTTCGA CCGGAAGAAA ACACCAAAAC TCACAACATAT ACCGAAGAAA ACCACATAT TCGCAGACTT 1620 135 AAAGAAGGAA ACCCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAAAACTCAA TCGCAGACTT 1680 136 AAAGAGAGAA ACCCTCACAT TAATTCAGA CCGGAAGAAA ACCACAAAACT TTAAAGATCC TAAATTCAGA CCGGAAGAAA ACCACAAACT TCACAACTAT ACCGAAGAAA ACCACAAACT TCACAACTAT ACCGAAGAAA ACTACTTTCC GAACAGAAAA ACCAAAACT TTAAATTCAGA CCGGAAGAAA ACTACTTTCC GAACAGAAAA ACCAAAACT TTAAATTCAGA CCGGAAGAAA ACTACTTTCC AAAAATTCAA AACTACTATA ACCTACACTT TAATTCAGA ACCAAAACT TCTCTTTTGCA ACAATTTAA TCACAAATTC 1680 145 CAAATGGAAG CAAGTTGGAC AACAAAACT TCTCTTTTGCA ACAATTCTA AACTTCTCT TAAATTCAGA AACAAAACTA TCTATTTTTA ACCATTTTC AACAATTCT AACTTCTCTA AACATCTTC AA	103 CCCAACTTCT CAACGAACTC TTGT	TCAATT TTGCGGGAAT AACGTTTTTG ATCATTTGAA 660
107 ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA GATCACTTTC TCAACAACAT 780 109 CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAAA ATATTTATT GCACTCATTT 840 111 TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTA AGTAACAAAA ACAATATTC 900 113 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATTCA AGAATATTA GAATTAGAAA 960 115 GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAAG TCAAAGATTT 10.20 117 TAACTTCAAC TACTATTTAA CAAAAATCTTG TCCTCTTCCA GAAAATTGGC GGGAACGGAA 1080 119 ACAAAAAATC GAAAACTTGA TAAATAAAAC CGTCACACAA TTTATTATATG AATTTTCTA 12.00 121 GCTGTTTAGC TACCAAACGT ATAATAAAAC CGTCACACAA TTTATTAATG AATTTTCTA 12.00 122 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCTT AGAGAATTTT AAAAGAAAAG	105 ACTCAACCAT AAGTTTGACA AAAA	GCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG 720
109 CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTATT GCACTCATTT 440 AGACGATGAC AGACCAATCT TCAAAAAGCA TGAGTTTGCA AGACTATATATA AGACTAAAAA ACAATATTTC 900 AGACGATGAC AGACCAAAAA ACAATATTCC 900 AGACGATGAC AGACCACAAA AGACTATATA AGACTAAAAA ACAATATTCC 900 AGACGACGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	107 ATCTTCATCA ACCTGCAAAT ACAA	TGTCAA GAATGAGAAA GATCACTTTC TCAACAACAT 780
111 TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTC 900 113 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATC AGATTTAATA GAATTAGAAA 960 115 GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT 1020 117 TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTTCCA GAAAATTGGC GGGAACGGAA 1080 119 ACAAAAAATC TAACTATTAA CAAAATCTTG TCCTCTTCCA GAAAATTGGC GGGAACGGAA 1080 110 ACAAAAAATC TAACACAACTG ATAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA 1140 111 GCTGTTTAGC TACACAACTG ATAATAAAAC CGTCACACAA TTTATTAATG AATTTTCTA 1200 112 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAAATTTC AAAAGAAAGT 1260 112 TAAGAAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC AAAAACTTAT TGCTTGAGAA 1320 113 CGTCGTCCG GAAAACATC ACGTCTTATG GAAATTGCC CGATGGATAT TCGAGGATCT 1440 114 CGTCGTCCG CTCAATAGAA ACACCTT ACGTCTATG GAAATTGCC CGATGGATAT TCGAGGATCT 1440 115 CAGACATTAC TACAGAAAGA ATATTTGGA CGTCATTATG AAAAGAAAAA GTTACTCCAA 1500 116 CAGACTTATAC ACGCTCAGA AAAAGAGGT GAACAAGAAAA ACAACTTAT TGCACCAGA AAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGAGT AAAAAGAGGT AAAAAGAGAGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGAGT AAAAAGAGAGT AAAAAGAGAGT AAAAAGAGAGT AAAAAGAGAGT AAAAAGAGAGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGGT AAAAAGAGAGT AAAAAGAGAGT AAAAAGAGAGT AAAAAGAGAGT AAAAAGAGAGT AAAAAGAGAGT AAAAAGAGAGT AAAAAGAGAGT AAAAAGAGGT AAAAAAGAGAGT AAAAAGAGAGT AAAAAGAGAGT AAAAAGAGAGT AAAAAGAGAGT AAAAAAACTAC AAAAAATAA CTACCAAAAATAC 1740 117 CGAAATGGAA CAGACTTATTA AACTACAAAACT CTTCTTTGCA AACAAAATAA CTACCAAAATAC 1740 118 CAGACTTATG AACTTCACT TAAATGAAA AACAATACA AACAAAATAA CTACCAAAATAC 1740 119 CAAATTGGAA AACAAAAACT CTTCTTTGCA AACAAATTAA CTACAAAATAC 1740 119 CAAATTGGAA AACAAAAACT CTTCTTTGCA AACAAATAC TAAAAAACTAC 1740 111 CAAATTGGAAAAC CTACAAAACT CTTCTTTGCA AACAATACA AACATACTA AATTACTTTC 1980 111 TTCGAAAAAC TTTAAAAAACAA AAAAACTACT AAAAATACA TAGTTATTCCAA AACAATACA AACAATACA AACAATACA AACAATACA AACAATACA AACAAAATAC TCTACAAAAATAC 1740 111 TTCGAAAAAC TTTAAAAAAAACAT AAC	100 CAACCTCCCG AATTGGAATA ATAT	GAAATC AAGAACCAGA ATATTTTATT GCACTCATTT 840
113 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA GAATTAGAAA 960 115 GAAGCTAAAA GATAAGGTTA TCGAAAAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT 1020 117 TAACTTCAAC TACTATTTAA CAAAATCTG TCCCTCTCCA GAAAATTGGC GGGAACGGAA 1080 119 ACAAAAAAATC GAAAACTGA TAAATAAAAC TAAGAGAAAA AAGTCGAAAGT ACTATGAAGA ATAATAAAAC CTCCAAAAAAAAATG CGTCACACAA TTTTATAATG AATTTTCTA 1200 121 GCTGTTTAGC TACACAACTG TTTTGACTGG AAGAAACCGT AAGAAATTTC AAAAAGAAAGT 1260 122 TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTATTCAC AAAAACTTAT TGCTTGAGAA 1320 127 GATCAATACA AGAGAAATAT CATGGATGCA GGTTGAGAC TCTGCAAAAC TTTTATTATA 1380 129 TTTTGATCAC GAAAACATCT ACGTCTTATG GAAATTGCC CGATGGATAT TCGAGGATCT 1440 131 CGTCGTCTG CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA 1500 133 AACCTATTCA TACAGAAAGA ATATTTGGA CGTCCAAGA AAAAGAGGAAA GTTACTCCAA 1500 134 AAGAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAAGAGGAAAA ACGCTTGCTG AGGTCCAAGAAA ACGCTTGCTG AGGTCCAAGAAA ACGCTTGCTG AGGTCCAAGAAAA ACGCTTGCTG AGGTCCAAGAAAA ACGCTTGCTG AGGTCCAAGAAAA ACGCTTGCTG AGGTCCAAGAAAA ACGCTTGCTG AGGTCCAAGAAAAACTATC AAGAAAACTATC AAGAAATTAA AGAAGAATG TAAATTCAGA CCGGAAGAAA ACTACTTCC GTCCAAATAC 1680 137 TGGATTTGCA CCTGGAAAAC TCAGACCAAAA ACCGAAGAAA ACTACTTCC GTCCAAATTAT 1680 143 TTTTGGATTC GCTGTTTTA ACCAAAACT CTTCTTTGCA ACAAAATTAA CTACAAATAC 1740 144 GAAGTTATTG AACTCCACT TAATGCTTAA GACATTGAAA AAAACTATC ACAAAATTAA CTACAAAATC 1740 145 CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA ACTATGGATA TCGAAAAATC 1740 146 GAAGTTATT TGGATTAGA CACCAAAACT CTTCTTTTGCA ACTATGGATA TCGAAAAAGTG 1920 147 ATATGATAGT GTAAACAGAG AACCAAAACT CTTCTTTTGCA ACTATGGATA TCGAAAAAGTG 1920 147 ATATGATAGT TTGGAACAGAG AAAAACTATC AACATTCCTA AAAACTACTA AATTACTTTC 1980 147 ATATGATAGT TTGGAACAGAG AAAAACTATC AACATTCCTA AAAACTACTA AATTACTTTC 1980 148 TTCGGAAAAAC TTTTAGAAAAC TTTAAAGAAAA AGAAATTAT AAAAACTACTA AATTACTTTC 1980 149 TTCGAAAAAC TTTTAGAAAACA AAAAACTATC AACATTACTTT AAAACAAAACTA TCCTAAAACAAAATGA 1100 151 TCCGAAAAAC TTTTAGAAAACA TAACTATCA AACAAAAACTA TCCTAAACAAAT TCCTAAACAAAA TTCTAAACAAAAACA AAGAAAATAAT TAATTATTT TAAGAAACA AAGAAAATGA AACAAAAACA AAGAAAA	111 TAATACAAAT AACCAATTCT TCAA	AAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC 900
115 GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT 117 TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTTCCA GAAAATTGGC GGGAACGGAA 1080 119 ACAAAAAATC GAAAACTGA TAAATAAAAC TAGAGAAGA AAGTCGAAGT ACTATGAAGA 1140 121 GCTGTTTAGC TACACAACTG ATAATAAAATG CGTCACACAA TTTATTAATG AATTTTCTA 1200 123 CAAATATACTC CCCAAAGACT TTTGACTGG AAGAAACCGT AAGAAATTTC AAAAGAAAAG	113 ACCCATGGAC AGAGCTCAGA CGAT	PATTCAC GAATATATTC AGATTTAATA GAATTAGAAA 960
117 TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTTCCA GAAAATTGGC GGGAACGGAA 1080 119 ACAAAAAATC GAAAACTTGA TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA 1140 121 GCTGTTTAGC TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA 1200 123 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAACCGT AAGAACTTTC AAAAGAAAGT 1260 125 TAAGAAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC AAAAACTTAT TGCTTGAGAA 1320 127 GATCAATACA AGAGAAATAT CATGGATGCA GGTTGAGACC TCTGCAAAGC ATTTTATTA 1380 129 TTTTGATCAC GAAAACATCT ACGCCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT 1440 131 CGTCGTCTCG CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA 1500 133 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGCAA TCGCAGACTT 1560 135 AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAACTATC AAAAACTTCC GTCCAATTAT 1680 139 GACTTTCAAT AAGAAGAATT TAAATTCAGA CCGGAAGACA ACTACTTTCC GTCCAATTAT 1680 141 GAAGTTATTG AACTCTCACT TAATGCTTAA GCCAAGAAAA ACTACTTTCC GTCCAATTAT 1680 142 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AACTACTAGAG AATTACTCTA 1800 143 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AACTACTAGAG AATTACTTTG 1860 145 CAAATGGAA CAAGTTGGAC AACCAAAACT TTTTTTTCAACAAAACT TTTAAAACAGA AACCATTCCTA AACAATAC 1740 146 CAAATGGAAACAT TAATGATGA CAACAAAACT TTTTTTTTCAACAAAACAT TCGAAAAACT TCGAAAAGTG 1920 147 ATATGATAGT GTAAACAGA AACACAACT TCTTTTTGCA ACCATAGAAA AACATTCCTA AAAACTACTA AATTACTTTC 1980 149 TTCAGATTC TGGATTATGA CTGCACAAAT TCTAAAGAGA AACAATACTA AATTACTTTC 1980 151 TCCGAAAAAC TTTAGAAAGA AAGAAACAT TCTAAAGAGA AAGAAATAC TAGTATACGA 2040 153 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAACCACA AAGAATTATT TTAAAGAAAGA 2220	115 GAACCTAAAA GATAAGGTTA TCGA	AAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT 1020
119 ACAAAAAATC GAAAACTTGA TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA 1200 121 GCTGTTTAGC TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA 1200 123 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTC AAAAGAAAGT 1260 125 TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTACTTCAC AAAAACTTAT TGCTTGAGAA 1320 127 GATCAATACA AGAGAAATAT CATGGATGCA GGTTGAGACC TCTGCAAAGC ATTTTATTA 1380 129 TTTTGATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT 1440 131 CGTCGTCTG CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA 1500 133 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGCAA TCGCAGACTT 1560 135 AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGA ACAACTCCT 1620 137 TGGATTTGCA CCTGGAAAAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT 1680 139 GACTTCAAT AAGAAGATG TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC 1740 141 GAAGTTATTG ACCTCACT TAATGCTTAA GACATTGAAG AATGAAATGA	117 TAACTTCAAC TACTATTTAA CAAA	ATCTTG TCCTCTTCCA GAAAATTGGC GGGAACGGAA 1080
121 GCTGTTTAGC TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA 123 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTC AAAAGAAAGT 125 TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC AAAAACTTAT TGCTTGAGAA 127 GATCAATACA AGAGAAATAT CATGGATGCA GGTTGAGACC TCTGCAAAGC ATTTTTATTA 1380 129 TTTTGATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT 131 CGTCGTCTCG CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA 133 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT 135 AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGAA ACGACTTATT 139 GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACA ACTACTTTCC GTCCAATTAT 141 GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGA TTAAAGACCCT 143 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAT TTAAAGATCC 143 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAT TCGAAAATAC 141 GAAGTTATTG CAAGTTGGAC AACCAAAACT CTTCTTTTGCA ACTATGAGA AGTTTGTTTG 1460 145 CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTTGCA ACTATGAGA AGTTTGTTTG 1460 147 ATATGATAGT GTAAACAGAG AAAAACCAT CTTCTTTTGCA ACTATGAGA AAGAATACA TAGTTATCCA 149 TTCAGATTC TGGATTATGA CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCCA 151 TTCGAAAAAC TTTAGAAAGA AAGAAATGAA AGAATTATT TCAGAAAATGA 1520 153 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAAATG AACAAAATGA 155 CTTAAATGCA AAGAAACAT TAATTGTTGA AGCAAAACTAT TTTAAGAAAGA 155 CTTAAATGCA AAGAAACAT TAATTGTTGA AGCAAAACTAT TTTAAGAAAGA 155 CTTAAATGCA AAGAAACAT TAATTGTTGA AGCAAAACTAT TTTAAGAAAGA 1520 153 TGCACTTGAA AAGAAAACAT TAATTGTTGA AGCAAAACTAT TTTAAGAAAGA 156 CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAACTAT TTTAAGAAAGA 156 CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAACTAT TTTAAGAAAGA 157 TTAAGAAAGA AAGAAAACAT TAATTGTTGA AGCAAAACTAT TTTAAGAAAGA AGCAAAACTAT TTTAAGAAAGA AGCAAAACTAT TTTAAGAAAGA AGCAAAACTAT TTTAAGAAAGA AGCAAAACTAT TTTAAGAAAGA AGCAAAACTAT TTTAAGAAAGA AGCAAAACTAT TTAATTATTT TTAAGAAAGA ACCAAAACTAT TTAATTGTTGA AGCAAAACTAT TTAATTATTT TTAAGAAAGA ACCAAAACTAT TAATTGTTGA AGCAAAACTAT TTAATTGTTTAAGCAAAACTAT TTAATTGTTGA AGCAAAACTAT TTAATTGTTGA AGCAAAACTAT TTAATTGTTGA AGCAAAACTAT T	119 ACAAAAATC GAAAACTTGA TAAA	TAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA 1140
123 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTC AAAAGAAAGT 1260 125 TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC AAAAACTTAT TGCTTGAGAA 1320 127 GATCAATACA AGAGAAATAT CATGGATGCA GGTTGAGACC TCTGCAAAGC ATTTTTATTA 1380 129 TTTTGATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT 1440 131 CGTCGTCTCG CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA 1500 133 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT 1560 135 AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGGA AAAAGTCGCT 1620 137 TGGATTTGCA CCTGGAAAAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT 1680 139 GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAAATAC 1740 141 GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGAATCC 1800 143 TTTTGGATTC GCTGTTTTA ACTATGATGA TGTAATGAAA AAGTATGAG AGTTTGTTTG	121 GCTGTTTAGC TACACAACTG ATAA	TAAATG CGTCACACAA TTTATTAATG AATTTTTCTA 1200
125 TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC AAAAACTTAT TGCTTGAGAA 1320 127 GATCAATACA AGAGAAATAT CATGGATGCA GGTTGAGACC TCTGCAAAGC ATTTTATTA 1380 129 TTTTGATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT 1440 131 CGTCGTCTCG CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA 1500 133 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT 1560 135 AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGGA AAAAGTCGCT 1620 137 TGGATTTGCA CCTGGAAAAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT 1680 139 GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC 1740 141 GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC 1800 143 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG AGTTTGTTT		
127 GATCAATACA AGAGAAATAT CATGGATGCA GGTTGAGACC TCTGCAAAGC ATTTTATTA 129 TTTTGATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT 131 CGTCGTCTCG CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA 133 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT 135 AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGGTT GAAGAATGGA AAAAGTCGCT 137 TGGATTTGCA CCTGGAAAAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT 139 GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC 141 GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC 143 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGA AGTTTGTTT		
129 TTTTGATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT 131 CGTCGTCTCG CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA 133 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT 135 AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGGA AAAAGTCGCT 137 TGGATTTGCA CCTGGAAAAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT 139 GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC 141 GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC 143 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG AGTTTGTTT	127 GATCAATACA AGAGAAATAT CATG	GATGCA GGTTGAGACC TCTGCAAAGC ATTTTTATTA 1380
131 CGTCGTCTCG CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA 133 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT 135 AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGGA AAAAGTCGCT 137 TGGATTTGCA CCTGGAAAAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT 139 GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC 141 GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC 143 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG AGTTTGTTT		
133 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT 135 AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGGA AAAAGTCGCT 137 TGGATTTGCA CCTGGAAAAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT 139 GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC 141 GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC 143 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG AGTTTGTTT	131 CGTCGTCTCG CTGATTAGAT GATT	TTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA 1500
135 AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGGA AAAAGTCGCT 137 TGGATTTGCA CCTGGAAAAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT 139 GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC 141 GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC 143 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG AGTTTGTTT	133 AACCTATTAC TACAGAAAGA ATAT	TTTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT 1560
137 TGGATTTGCA CCTGGAAAAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT 1680 139 GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC 1740 141 GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC 1800 143 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG AGTTTGTTT	135 AAAGAAGGAA ACGCTTGCTG AGGT	CCAAGA AAAAGAGGTT GAAGAATGGA AAAAGTCGCT 1620
139 GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC 141 GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC 143 TTTTGGATTC GCTGTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG AGTTTGTTT	137 TGGATTTGCA CCTGGAAAAC TCAG	SACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT 1680
141GAAGTTATTGAACTCTCACTTAATGCTTAAGACATTGAAGAATAGAATGTTTAAAGATCC143TTTTGGATTCGCTGTTTTAACTATGATGATGTAATGAAAAAGTATGAGGAGTTTGTTTG1860145CAAATGGAAGCAAGTTGGACAACCAAAACTCTTCTTTGCAACTATGGATATCGAAAAGTG1920147ATATGATAGTGTAAACAGAGAAAAACTATCAACATTCCTAAAAAACTACTAAATTACTTTC1980149TTCAGATTTCTGGATTATGACTGCACAAAATTCTAAAGAGAAAGAATAACATAGTTATCGA2040151TTCGAAAAACTTTAGAAAGAAAGAAATGAAAGATTATTTTAGACAGAAATTCCAGAAGAT2100153TGCACTTGAAGGAGGACAATATCCAACCTTATTCAGTGTTCTTGAAAAATGAACAAAAATGA2160155CTTAAATGCAAAGAAAACATTAATTGTTGAAGCAAAGCAAAGAAATTATTTTAAGGAAAGA2220	139 GACTTTCAAT AAGAAGATTG TAAA	ATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC 1740
143TTTTGGATTCGCTGTTTTTAACTATGATGATGTAATGAAAAAGTATGAGGAGTTTGTTTG1860145CAAATGGAAGCAAGTTGGACAACCAAAACTCTTCTTTGCAACTATGGATATCGAAAAGTG1920147ATATGATAGTGTAAACAGAGAAAAACTATCAACATTCCTAAAAACTACTAAATTACTTTC1980149TTCAGATTTCTGGATTATGACTGCACAAAATTCTAAAAGAGAAGAATAACATAGTTATCGA2040151TTCGAAAAACTTTAGAAAGAAAGAAATGAAAGAATTATTTAGACAGAAATTCCAGAAGAT153TGCACTTGAAGGAGGACAATATCCAACCTTATTCAGTGTTCTTGAAAAATGAACAAAAATGA2160155CTTAAATGCAAAGAAAACATTAATTGTTGAAGCAAAGCAAAGAAATTATTTTAAGAAAGA2220	141 GAAGTTATTG AACTCTCACT TAAT	GCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC 1800
145CAAATGGAAGCAAGTTGGACAACCAAAACTCTTCTTTGCAACTATGGATATCGAAAAGTG1920147ATATGATAGTGTAAACAGAGAAAAACTATCAACATTCCTAAAAACTACTAAATTACTTTC1980149TTCAGATTTCTGGATTATGACTGCACAAAATTCTAAAGAGAAAGAATAACATAGTTATCGA2040151TTCGAAAAACTTTAGAAAGAAAGAAATGAAAGATTATTTTAGACAGAAATTCCAGAAGAT2100153TGCACTTGAAGGAGGACAATATCCAACCTTATTCAGTGTTCTTGAAAAATGAACAAAAATGA2160155CTTAAATGCAAAGAAAACATTAATTGTTGAAGCAAAGCAAAGAAATTATTTTAAGAAAGA2220	143 TTTTGGATTC GCTGTTTTTA ACTA	TGATGA TGTAATGAAA AAGTATGAGG AGTTTGTTTG 1860
147ATATGATAGTGTAAACAGAGAAAAACTATCAACATTCCTAAAAACTACTAAATTACTTTC1980149TTCAGATTTCTGGATTATGACTGCACAAATTCTAAAAGAGAAGAATAACATAGTTATCGA2040151TTCGAAAAACTTTAGAAAGAAAGAAATGAAAGATTATTTTAGACAGAAATTCCAGAAGAT153TGCACTTGAAGGAGGACAATATCCAACCTTATTCAGTGTTCTTGAAAAATGAACAAAATGA155CTTAAATGCAAAGAAAACATTAATTGTTGAAGCAAAGCAAAGAAATTATTTTAAGAAAGA	145 CAAATGGAAG CAAGTTGGAC AACC	CAAAACT CTTCTTTGCA ACTATGGATA TCGAAAAGTG 1920
149 TTCAGATTTC TGGATTATGA CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA2040151 TTCGAAAAAC TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT2100153 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG AACAAAATGA2160155 CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA	147 ATATGATAGT GTAAACAGAG AAAA	ACTATC AACATTCCTA AAAACTACTA AATTACTTTC 1980
151 TTCGAAAAAC TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT 153 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG AACAAAATGA 155 CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA	149 TTCAGATTTC TGGATTATGA CTGC	CACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA 2040
153 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG AACAAAATGA 2160 155 CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA	151 TTCGAAAAAC TTTAGAAAGA AAGA	AAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT 2100
155 CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA	153 TGCACTTGAA GGAGGACAAT ATCC	CAACCTT ATTCAGTGTT CTTGAAAATG AACAAAATGA 2160
	155 CTTAAATGCA AAGAAAACAT TAAT	TTGTTGA AGCAAAGCAA AGAAATTATT TTAAGAAAGA 2220
157 TAACTTACTT CAACCAGTCA TTAATATTTG CCAATATAAT TACATTAACT TTAATGGGAA 2280	157 TAACTTACTT CAACCAGTCA TTAA	ATATTTG CCAATATAAT TACATTAACT TTAATGGGAA 2280

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	159	GTTTTATAA	A CA	AACA	AAAG	GAA	TTCC	TCA	AGGT	CTTT	GA G	ТТТС	ATCA	A TT	TTGT	CATC		2340
	161	ATTTTATTA	T GC	AACA	TTAG	AGG	AAAG	CTC	CTTA	GGAT	TC C	TTAG	AGAT	G AA	TCAA	TGAA		1:400
	163	CCCTGAAAA	т сс	AAAT	'GTTA	ATC	TTCT	AAT	GAGA	CTTA	CA G	ATGA	CTAT	C TT	TTGA	TTAC		2460
	165	AACTCAAGA	G AA	ТААТ	'GCAG	TAT	TGTT	TAT	TGAG	AAAC	TT A	TAAA	CGTA	A GT	CGTG	AAAA		2520
	167	TGGATTTAA	A Trif	CAAT	'AΤGA	AGA	AACT	ACA	GACT	AGTT	TT C	CATT	AAGT	C CA	.AGCA	AATT		2580
	160	TGCAAAATA	e gg	AATG	GATA	GTG	TTGA	GGA	GCAA	AATA	TT G	TTCA	AGAT	T AC	TGCG	ATTG		2640
	171	GATTGGCAT	CTC	ΊΑΑΤΤ	'GATA	TGA	AAAC	TCT	TGCT	TTAA	TG C	CAAA	TATT	A AC	TTGA	GAAT		2700
	172	AGAAGGAAT	т <i>С</i> т	GTGT	ACAC	TCA	ATCT	AAA	CATG	CAAA	CA A	AGAA	AGCA	T CA	ATGT	GGCT		2760
	175	CAAGAAGAA	A CT	ΙΔΙΔΙ	тсст	י ידידי	TAAT	GAA	TAAC	ATTA	.cc c	ATTA	TTTT	'A GA	AAGA	CGAT		2820
	177	TACAACCGA	Λ CΔ	ייייייי <i>יי</i> י.	GCGA	АТА	AAAC	тст	CAAC	AAGT	TA I	TATT	ATCA	.G GC	GGTT	ACAA		2880
	170	ATACATGCA	.д. О/: Л Tra	AGCC	ΊΔΔΔΟ	ΤΑΔ :	ACAA	GGA	CCAC	TTTA	AG A	AGAA	CTTA	G CI	'ATGA	GCAG		2940
	101	TATGATCGA	ייג בא. דידו יי	NGAG	CTAT	ста	TAAA	TAT	ATAC	TCTG	TA A	CCAG	AGCA	т то	TTTA	AATA		3000
	107	CCTTGTGTG	מג כי.	. תטבע דית גית	A A C C	ι ΔπΔ	CAAT	היחים	TGGA	GAGG	AG C	ATTA	TCCA	G AC	TTTT	TCCT	1	3060
	105	TAGCACACT	C AM	CCAC	מטרא. מחידיתי	. ጥጥ <i>ር</i>	ΙΔΔΔΊ	חידים	CAGC	ACAA	AA A	AGTA	CATI	т то	CAACA	GAGT	1	3120
	102	TTGCATGAT	א כי	DA A DE	ירים זרים א	1 110	AACC	מממי	GCTA	AAAA	GT 6	ACCA	ATGI	'C AA	TCTC	TAAT	1	3180
	100	TCAATATGA	TO CA	יט אמט. מידי אי	190A2		, ттСт	ΊΔΑς	TTAT	тттс	GA A	AGTI	TTAA	т то	CAATT	TTTG	;	3240
	189	TCTTATATA	יו פר	CCCT	naman. Stoot	CGG	ւրարարա	rece	GTTT	TGGG	iG.							3279
		(2) INFOR								1000								
		(2) INFOR	CEOU	ON E	E CH	יייע מיי	ידסדים ידסדים	7. Z.										
	195	(1)	SEVU	TENCE	i Ciir	103	ti an	ni no	acid	S								
	196				PE: 6				aoro									
	197		(0)	CUL	DANIDI	TOMES	id. N	iot i	Relev	rant								
	198 199				POLO					411 0								
>	201	(ii)							·unc									
	201	(xi)	CEOU	IENCE	DES	CRIE	ттог	ı. SI	EO TE	NO:	2:							
	205	(XI)	Clu	Val	Aen Aen	Val	Agn	Asn	Gln	Ala	Asp	Asn	His	Gly	Ile	His	Ser	
	205	1	GLU	vui	тор	5	DF				10			_		15		
	208	1 λ1a	Len	Lvs	Thr	Cvs	Glu	Glu	Ile	Lvs	Glu	Ala	Lys	Thr	Leu	Tyr	Ser	
	209		пса	LIU	20	012				25			_		30			
	211	Trn	Tle	Gln	Lvs	Val	Ile	Arq	Cys	Arq	Asn	Gln	Ser	Gln	Ser	His	Tyr	
	212			35					40					45				
	214	Lvs	Asp	Leu	Glu	Asp	Ile	Lys	Ile	Phe	Ala	Gln	Thr	Asn	Ile	Val	Ala	
	215		50					55					60					
	217	Thr	Pro	Ara	Asp	Tyr	Asn	Glu	Glu	Asp	Phe	Lys	Val	Ile	Ala	Arg	Lys	
	218	65					7.0					75					80	
	220	Glu	Val	Phe	Ser	Thr	Gly	Leu	Met	Ile	Glu	Leu	Ile	Asp	Lys	Cys	Leu	
	221					85					90					95		
	223	Val	Glu	Leu	Leu	Ser	Ser	Ser	Asp	Val	Ser	Asp	Arg	Gln	Lys	Leu	Gln	
	224				100					105					110			
	226	Cvs	Phe	Gly	Phe	Gln	Leu	Lys	Gly	Asn	Gln	Leu	Ala	Lys	Thr	His	Leu	
	227			115					120					125				
	229	Leu	Thr	Ala	Leu	Ser	Thr	Gln	Lys	Gln	Tyr	Phe	Phe	Gln	Asp	Glu	Trp	
	230		130					135					140					
	232		Gln	Val	Ara	Ala	Met	Ile	Gly	Asn	Glu	Leu	Phe	Arg	His	Leu	Tyr	
	233	145					150					155					160	
	235		Lvs	Tyr	Leu	Ile	Phe	Gln	Arg	Thr	Ser	Glu	Gly	Thr	Leu	Val	Gln	
	236					165					170					175		
	238	Phe	Cvs	Glv	Asn	Asn	Val	Phe	Asp	His	Leu	Lys	Val	Asn	Asp	Lys	Phe	
	239		- 1 -	1	180				_	185					190			

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									_			_		_	_	_
241	Asp	Lys	_	Gln	Lys	Gly	Gly		Ala	Asp	Met	Asn	Glu	Pro	Arg	Cys
242			195					200		_	~ 1	_	205		nl .	•
244	Cys	Ser	Thr	Cys	Lys	Tyr		Val	Lys	Asn	Glu		Asp	His	Phe	Leu
245		210					215					220	_		m.1	
247	Asn	Asn	Ile	Asn	Váil		Asn	Trp	Asn	Asn		Lys	Ser	Arg	Thr	
248	225					230					235	- 1	1	- 1	_	2.10
250	Ile	Phe	Tyr	Cys		His	Phe	Asn	Arg		Asn	Gln	Phe	Phe		Lys
251					245					250					255	- 1
253	His	Glu	Phe		Ser	Asn	Lys	Asn		He	Ser	Ala	Met		Arg	Ala
254				260					265			_	- 1	270	_	_
256	Gln	Thr		Phe	Thr	Asn	Ile		Arg	Phe	Asn	Arg	Ile	Arg	Lys	Lys
257			275					280					285		_	
259	Leu	_	Asp	Lys	Val	Ile		Lys	Ile	Ala	Tyr		Leu	Glu	Lys	Vai
260		290					295					300	_	_	_	_
262	Lys	Asp	Phe	Asn	Phe		Tyr	Tyr	Leu	Thr		Ser	Cys	Pro	Leu	
263	305					310					315			_ 3		320
265	Glu	Asn	Trp	Arg		Arg	Lys	Gln	Lys		Glu	Asn	Leu	Ile		Lys
266					325					330	_			_	335	_,
268	Thr	Arg	Glu	Glu	Lys	Ser	Lys	Tyr		Glu	Glu	Leu	Phe		Tyr	Thr
269				340					345					350	_	_
271	Thr	Asp	Asn	Lys	Cys	Val	Thr		Phe	Ile	Asn	Glu	Phe	Phe	Tyr	Asn
272			355					360				_	365	_	n.1	a.1
274	Ile		Pro	Lys	Asp	Phe		Thr	Gly	Arg	Asn		Lys	Asn	Phe	GIn
275		370					375	_				380	~ 3	_	- 1	1
277		Lys	Val	Lys	Lys		Val	Glu	Leu	Asn		His	Glu	Leu	Пе	
278	385					390		_			395			~	_	400
280	Lys	Asn	Leu	Leu		Glu	Lys	Ile	Asn		Arg	Glu	Ile	Ser		мет
281					405					410	_	m.1	_		415	
283	Gln	Val	Glu		Ser	Ala	Lys	His		Tyr	Tyr	Phe	Asp		GIU	Asn
284				420					425	_		-1		430	.	**- 1
286	Ile	Tyr		Leu	Trp	Lys	Leu		Arg	Trp	шe	Pne	Glu	Asp	Leu	Val
287			435				_,	440	_	1	an l	a 1	445	a1	T ~	C
289	Val		Leu	Ile	Arg	Cys		Pne	Tyr	Val	Thr		Gln	GIN	Lys	ser
290		450			_	_	455	_	.		T1 -	460	7 ~~	1707	т1.	Mat
292	_	Ser	Lys	Thr	Tyr		Tyr	Arg	Lys	Asn		Trp	Asp	Val	rre	
293	465		_			470	_		_	a.1	475	T	77.	a 1	170 1	480
295	Lys	Met	Ser	He		Asp	Leu	Lys	Lys		Thr	ьeu	Ala	GIU		GIII
296					485	- 3		_	-	490	.	a 1	73 la -	71-	495	C1
298	Glu	Lys	Glu	Val	Glu	Glu	Trp	Lys	Lys	Ser	Leu	СТА	Phe			GIY
299														510		m l
301	Lys	Leu		Leu	Ile	Pro	Lys		Thr	Thr	Pne	Arg	Pro	тте	мет	THE
302			515	_	_,		_	520	_	•	T	m la	525	T	т о	m b x
304	Phe		Lys	Lys	He	۷al		ser	Asp	arg	LУS		Thr	гаг	ьeu	TIII
305	_	530	_•	_	_	_	535			_	34 - 4	540	T	m 1	t	T ~
307		Asn	Thr	Lys	Leu		Asn	Ser	His	Leu		ьeu	Lys	rnr	ьeu	
308	545	_		5. 2	_	550	5	D.1	01 -	D.I	555	37-7	nh -	7~~	m~	560
310	Asn	Arg	Met	Phe		Asp	Pro	ьиe	GTÀ		АТа	val	Phe	ASI	TÄL	ASP
311				_	565	_		a 2	n!	570	Qr	T	m	T	575	1/2 1
313	Asp	Val	Met	Lys	Lys	Tyr	Glu	Glu	Phe	val	Cys	гÀг	Trp	ьys	GTIJ	٧d⊥

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0.7.4				E00					585					590		
314	a 1	C15	D *: 0	580	T OU	Dho	Dho	Ala		Mot	Agn	Tle	Glu		Cvs	Tvr
316	GIĀ	GIII		гуѕ	Leu	PHE	Phe	600	1111	MCC	изь	110	605	1112	015	- 1 -
317		<i>a</i>	595	7	7 22 0	Clu	Lvc	Leu	Cor	Thr	Dho	Lou		Thr	Thr	Lvs
319	Asp		val	ASII	AIG	GIU	615	Leu	261	1 111	FIIC	620	Буб	1111	1111	D _I U
320	_	610	G	G	1	Dha		Tlo	Mot	Thr	λla		Tlo	Τ.Δ.11	Lve	Δrσ
322		Leu	Ser	ser	Asp		trb	Ile	мес	TIII	635	GIII	116	пец	цуз	640
323	625	_	_	+ 1	1	630	7	C	Tira	7 an		λνα	Tuc	Tvc	Clu	
325	Lys	Asn	Asn	He		ite	Asp	Ser	ьуѕ		PHE	AIG	цуѕ	цуз	655	Mec
326				,	645	~ 1	_	- 1	a1.	650	т1.	7] -	T 0.1	C1.,		C111
328	Lys	Asp	Tyr		Arg	GIn	Lys	Phe		гуѕ	тте	Ald	Leu		GIY	GLY
329				660				1	665	a 1	_	a 1	a1	670	3	т
331	Gln	Tyr		Thr	Leu	Phe	Ser	Val	Leu	GIU	Asn	GIU		ASII	ASP	Leu
332			675				_	680			_	a 1	685			nl
334	Asn	Ala	Lys	Lys	Thr	Leu		Val	GLu	Ala	Lys		Arg	Asn	Tyr	Pne
335		690					695			_		700	_	~ 1	_	_
337	Lys	Lys	Asp	Asn	Leu		Gln	Pro	Val	He		He	Суѕ	GIn	Tyr	
338	705					710					715	_				720
340	Tyr	Ile	Asn	Phe	Asn	Gly	Lys	Phe	Tyr		Gln	Thr	Lys	Gly		Pro
341					725					730		_			735	_,
343	Gln	Gly	Leu	Cys	Val	Ser	Ser	Ile		Ser	Ser	Phe	Tyr		Ala	Thr
344				740					745					750		
346	Leu	Glu	Glu	Ser	Ser	Leu	Gly	Phe	Leu	Arg	Asp	Glu		Met	Asn	Pro
347			755					760					765			
349	Glu	Asn	Pro	Asn	Val	Asn	Leu	Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu
350		770					775					780				
352	Leu	Ile	Thr	Thr	Gln	Glu	Asn	Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu
353	785					790					795					800
355	Ile	Asn	Val	Ser	Arg	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys		Leu
356					805					810					815	
358	Gln	Thr	Ser	Phe	Pro	Leu	Ser	Pro	Ser	Lys	Phe	Ala	Lys		Gly	Met
359				820					825					830		
361	Asp	Ser	Val	Glu	Glu	Gln	Asn	Ile	Val	Gln	Asp	Tyr	Cys	Asp	Trp	Ile
362			835					840					845			
364	Gly	Ile	Ser	Ile	Asp	Met	Lys	Thr	Leu	Ala	Leu	Met	Pro	Asn	Ile	Asn
365		850					855					860				
367	Leu	Arg	Ile	Glu	Gly	Ile	Leu	Cys	Thr	Leu	Asn	Leu	Asn	Met	Gln	
368	865					870					875					880
370	Lys	Lys	Ala	Ser	Met	Trp	Leu	Lys	Lys	Lys	Leu	Lys	Ser	Phe	Leu	Met
371	_				885					890					895	
373	Asn	Asn	Ile	Thr	His	Tyr	Phe	Arg	Lys	Thr	Ile	Thr	Thr	Glu	Asp	Phe
374				900					905					910		
376	Ala	Asn	Lys	Thr	Leu	Asn	Lys	Leu	Phe	Ile	Ser	Gly	Gly	Tyr	Lys	Tyr
377			915					920					925			
379	Met	Gln	Cys	Ala	Lys	Glu	Tyr	Lys	Asp	His	Phe	Lys	Lys	Asn	Leu	Ala
380		930			4		935	•	-			940				
382	Met			Met	Ile	Asp	Leu	Glu	Val	Ser	Lys	Ile	Ile	Tyr	Ser	Val
383	945					950					955					960
385			Ala	Phe	Phe	Lys	Tyr	Leu	Val	Cys	Asn	Ile	Lys	Asp	Thr	Ile
386		5	-	_	965		•			970					975	
555																

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L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:199 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=2
L:479 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4
L:596 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=5
L:715 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=6
L:832 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=7
L:979 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=8
L:1156 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=9
L:1185 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=10
L:1218 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=11
L:1248 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=12
L:1280 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=13
L:1307 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=14
L:1334 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=15
L:1361 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=16
L:1388 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17
L:1415 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=18
L:1439 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=19
L:1463 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=20
L:1487 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=21
L:1511 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=22
L:1534 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23
L:1555 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=24
L:1576 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=25
L:1597 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=26
L:1618 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=27
 L:2336 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=54
 L:2513 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=55
 L:2723 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=58
 L:2744 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=59
 L:3287 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 68
 L:3415 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 68
 L:3511 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 68
 L:3777 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=70
 L:3805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
 L:3816 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=72
 L:3843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
 L:3854 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=74
 L:3882 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
 L:3893 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=76
 L:3926 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=78
 L:4390 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=87
 L:4405 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=88
 L:4420 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=89
 L:4436 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=90
 L:4451 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=91
 L:4467 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=92
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L:4483 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=93
L:4499 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=94
L:4515 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=95
L:4531 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=96
L:4547 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=97
L:4563 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=98
L:4579 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=99
L\!:\!4722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101
L:4820 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=102
L:4836 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=103
L:4851 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=104
L\!:\!6626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6629 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6644 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6711 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:176
L:6730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:177
L\!:\!6733 M\!:\!341 W: (46) "n" or "Xaa" used, for SEQ ID#:177
L:6929 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:185
L:7302~M:341~W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:203
L:7373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:203
L:7495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206
L:7748 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:7751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:7768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216
L:7771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216
L:7796\ M:341\ W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7799 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L\!:\!7805~M\!:\!341~W\!: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7832 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7913 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
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